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FIG. 1A

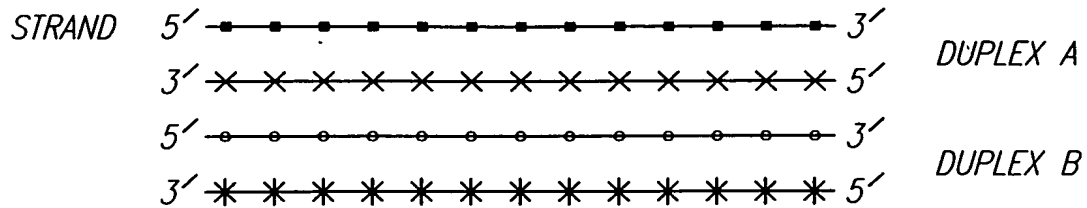


FIG. 1B

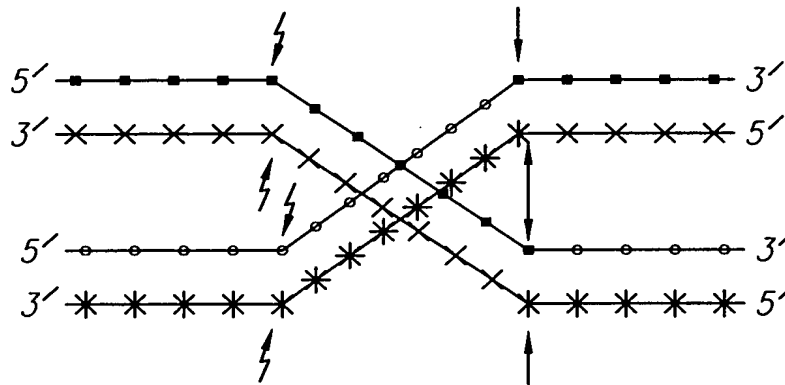
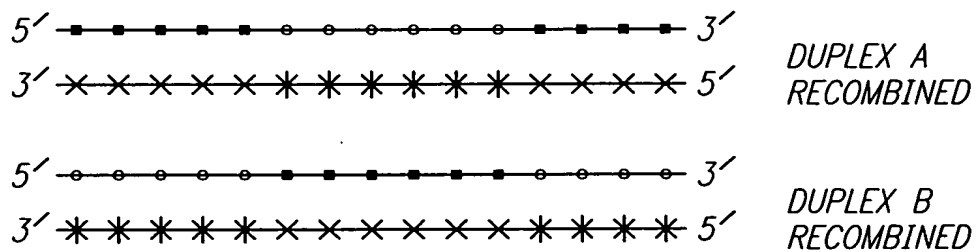


FIG. 1C



■ 5' TO 3' DNA SEGMENT 1
 × 3' TO 5' DNA SEGMENT 1
 ○ 5' TO 3' DNA SEGMENT 2
 * 3' TO 5' DNA SEGMENT 2

DUPLEX A

DUPLEX B

↓ STRAND BREAK + LIGATION

⚡ CUT SITE + LIGATION

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FIG. 3

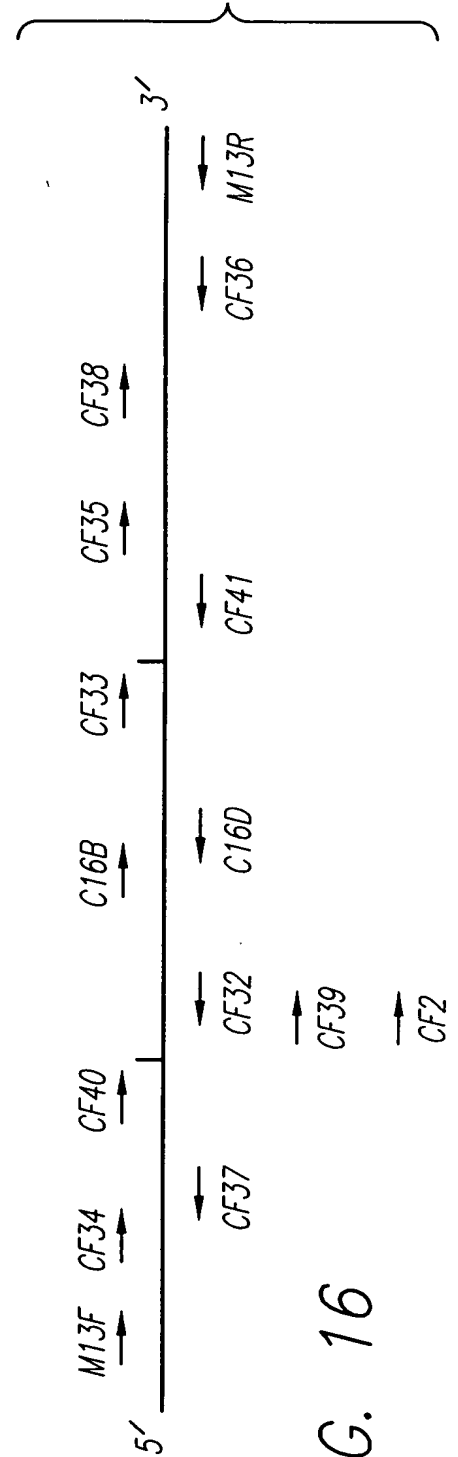
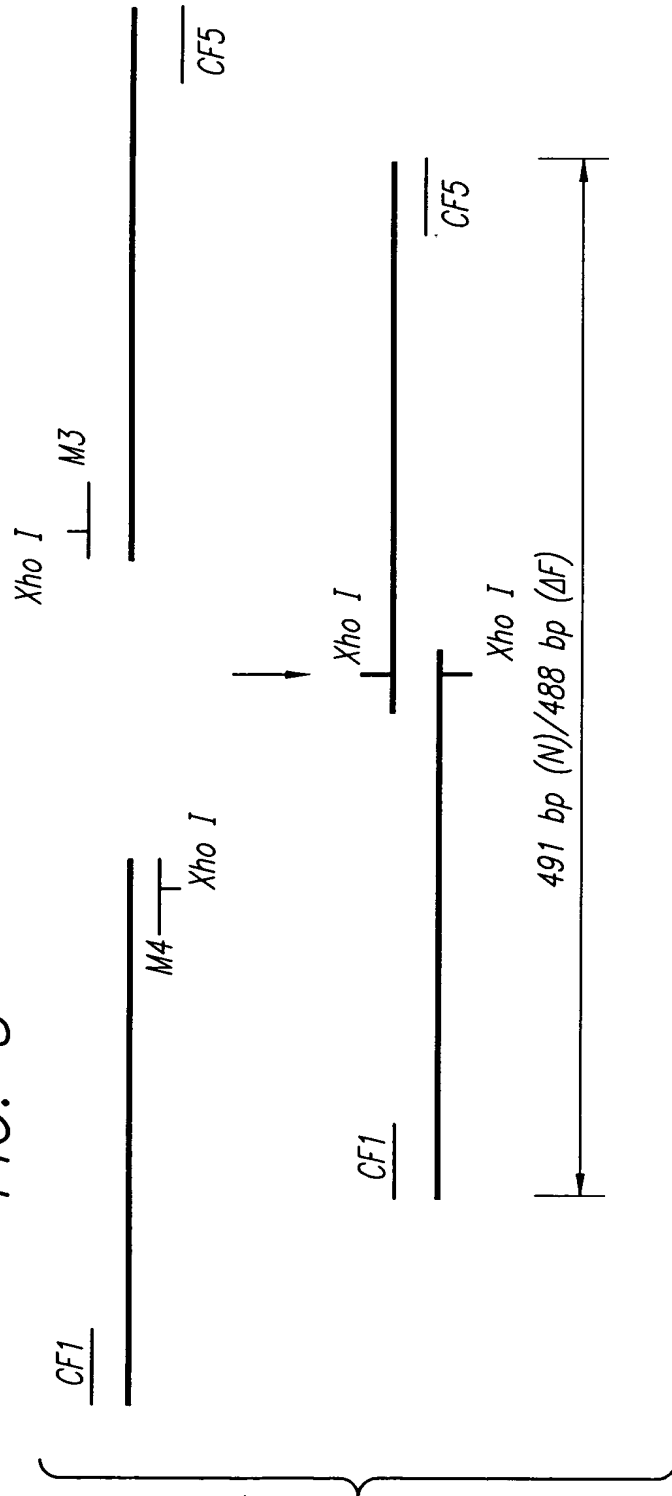


FIG. 16

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIG. 6A

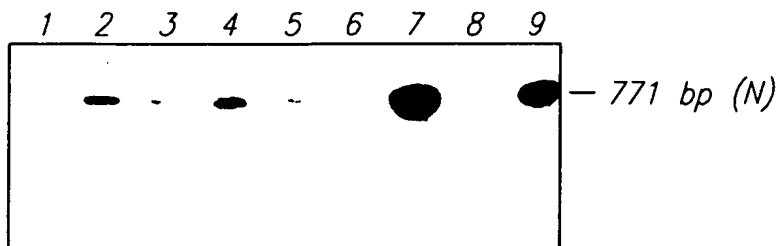


FIG. 6B

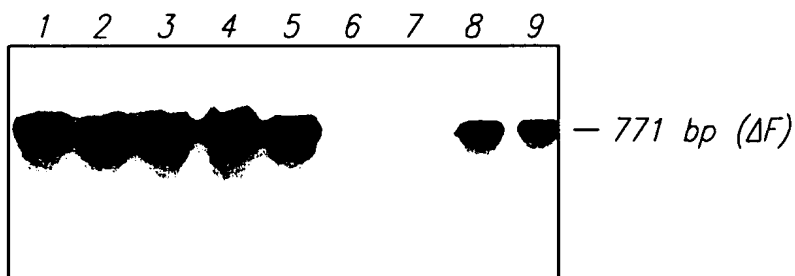


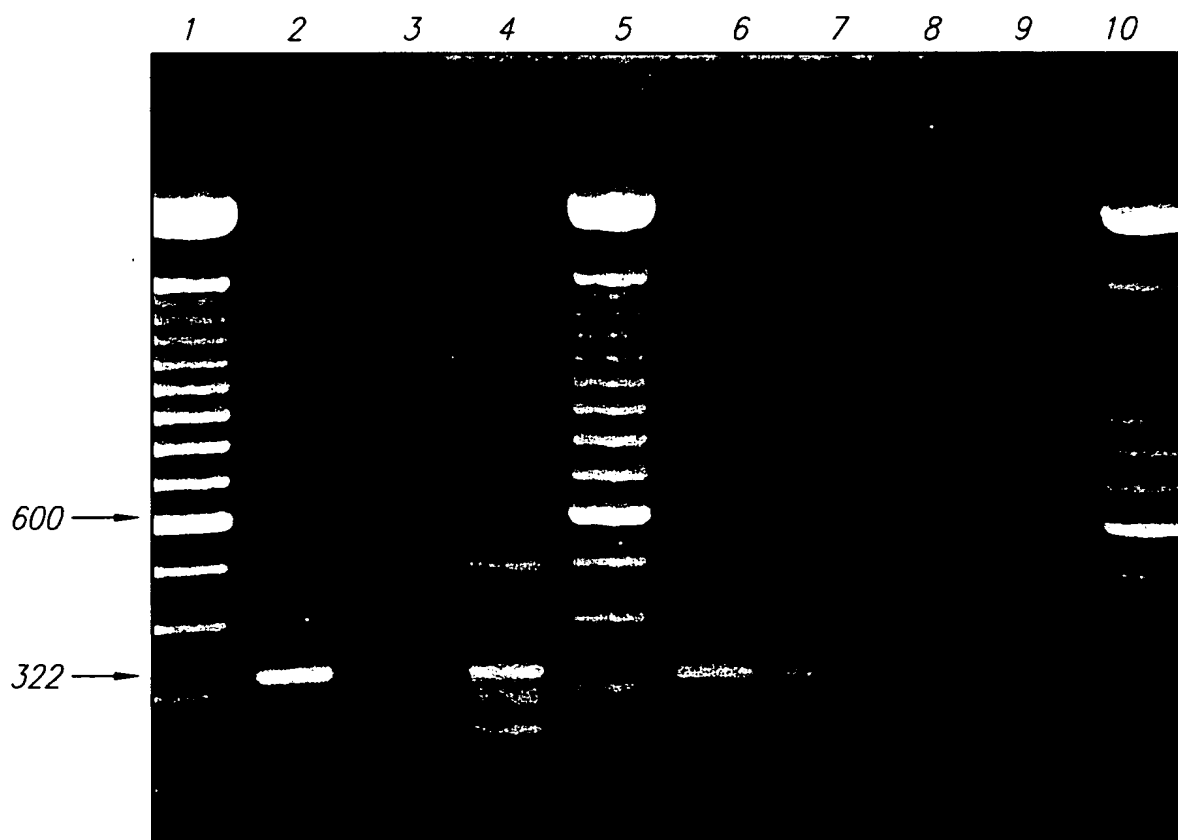
FIG. 7A



FIG. 7B

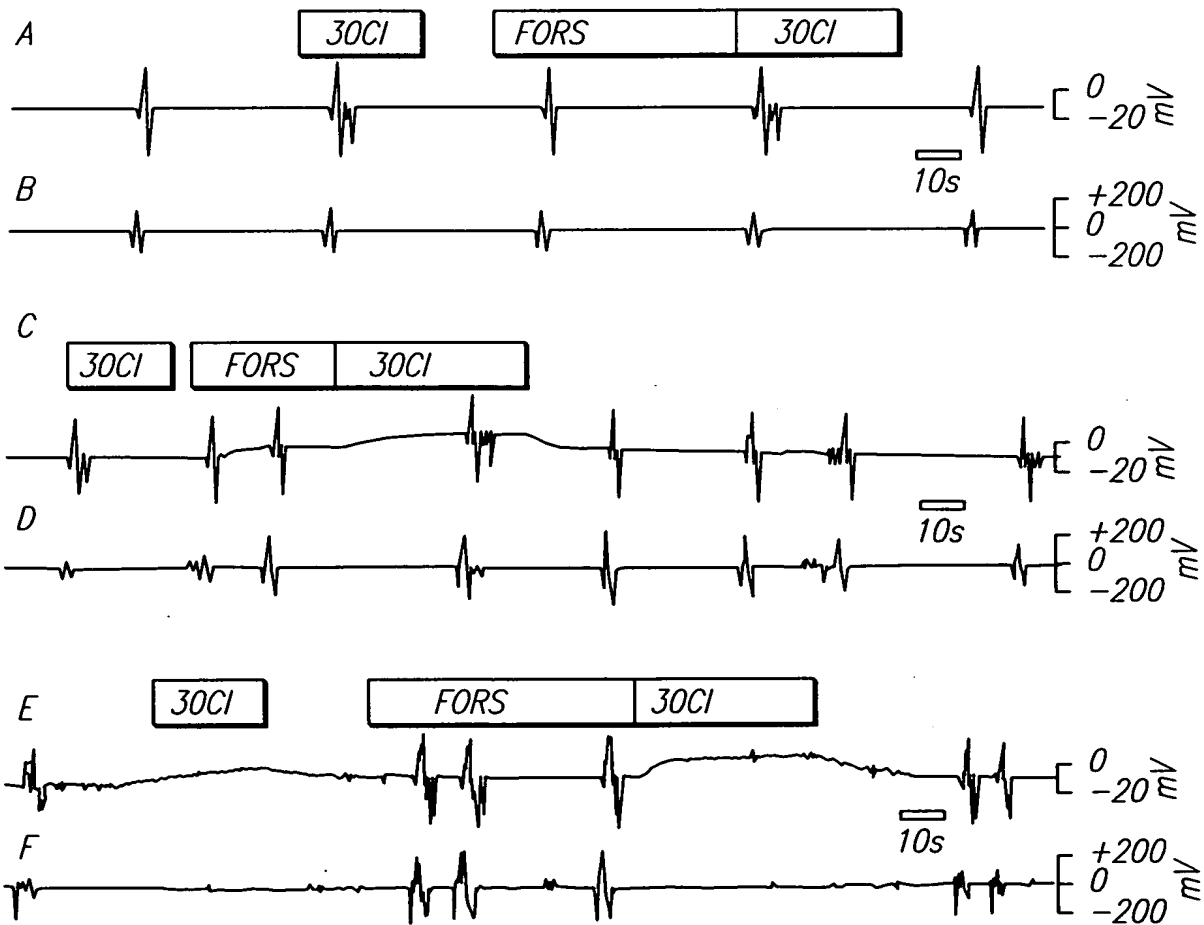
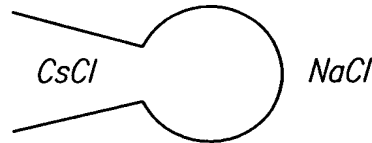
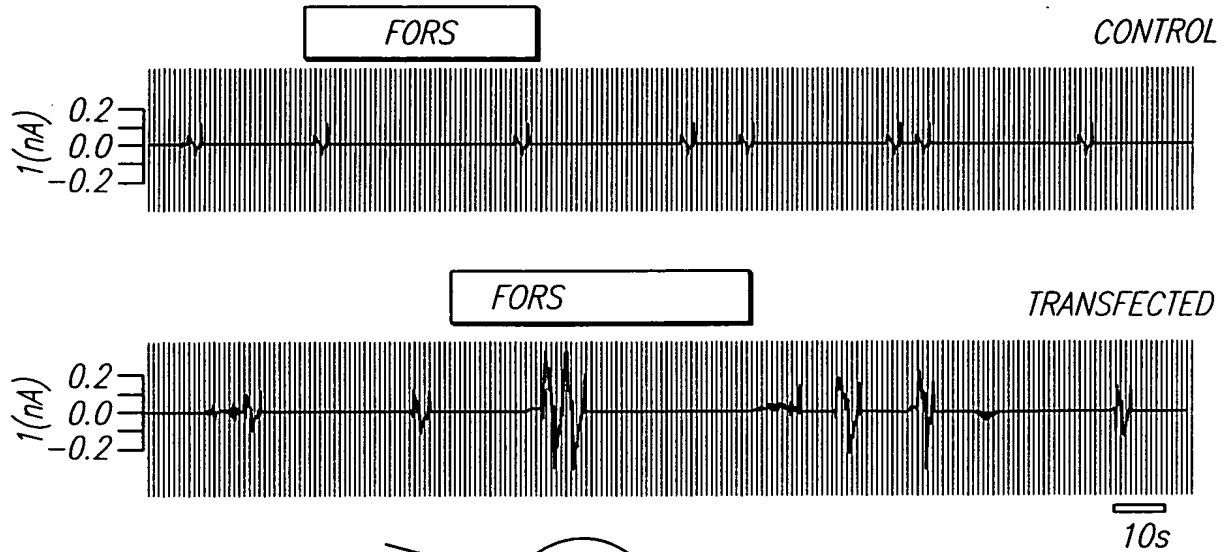


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FIG. 11



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FIG. 12

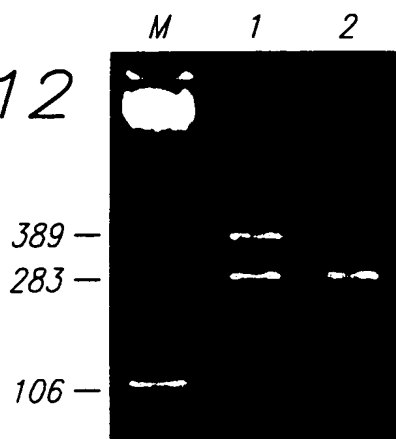


FIG. 13

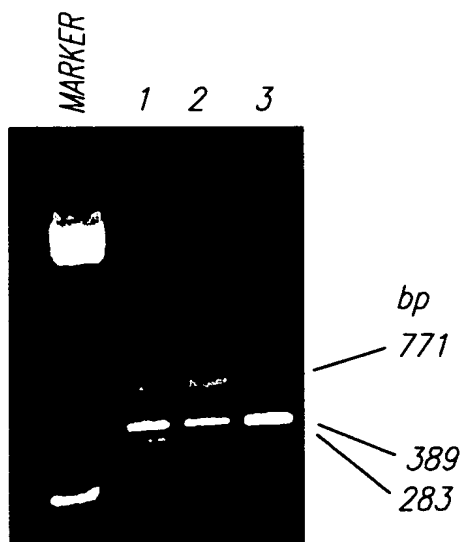
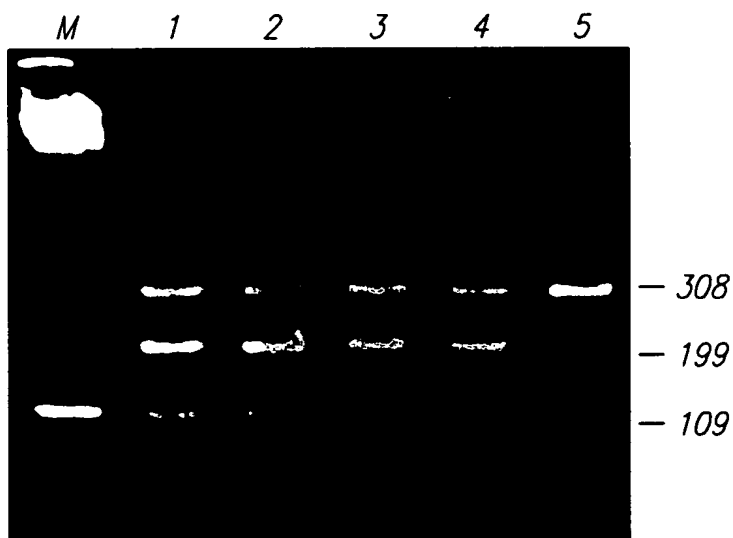


FIG. 14



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FIG. 18

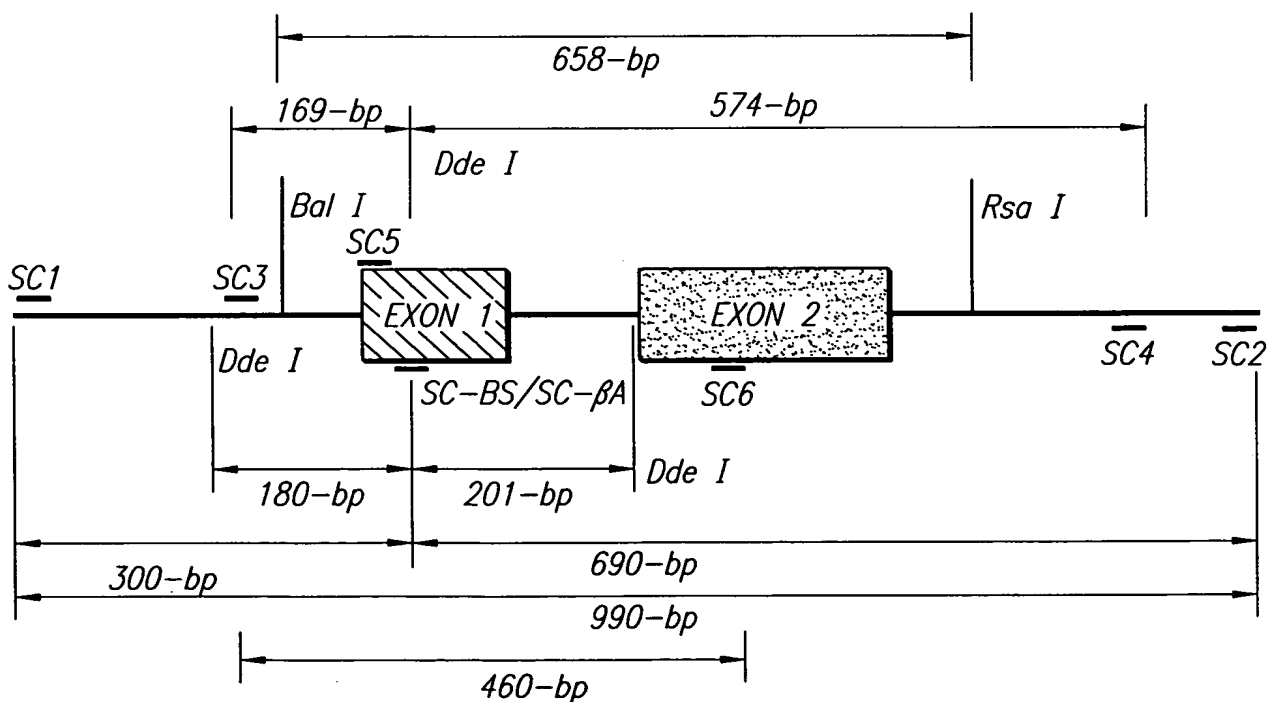
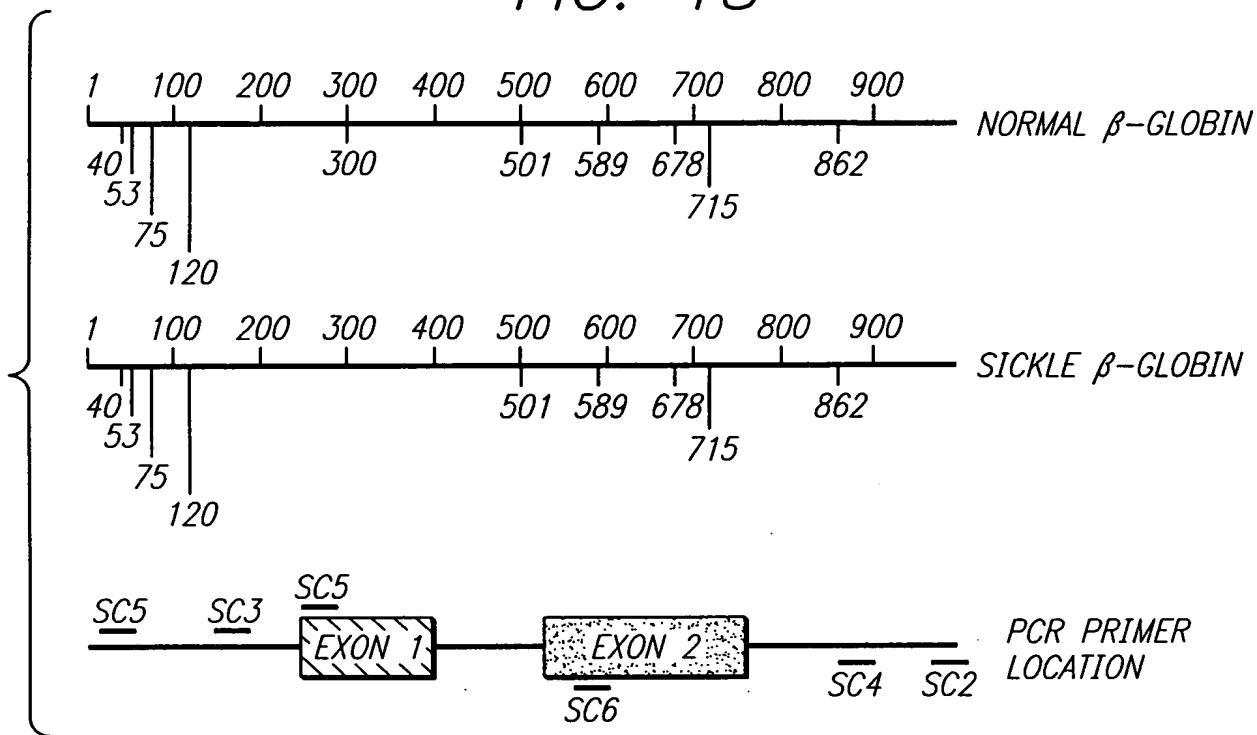


FIG. 19

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FIG. 20

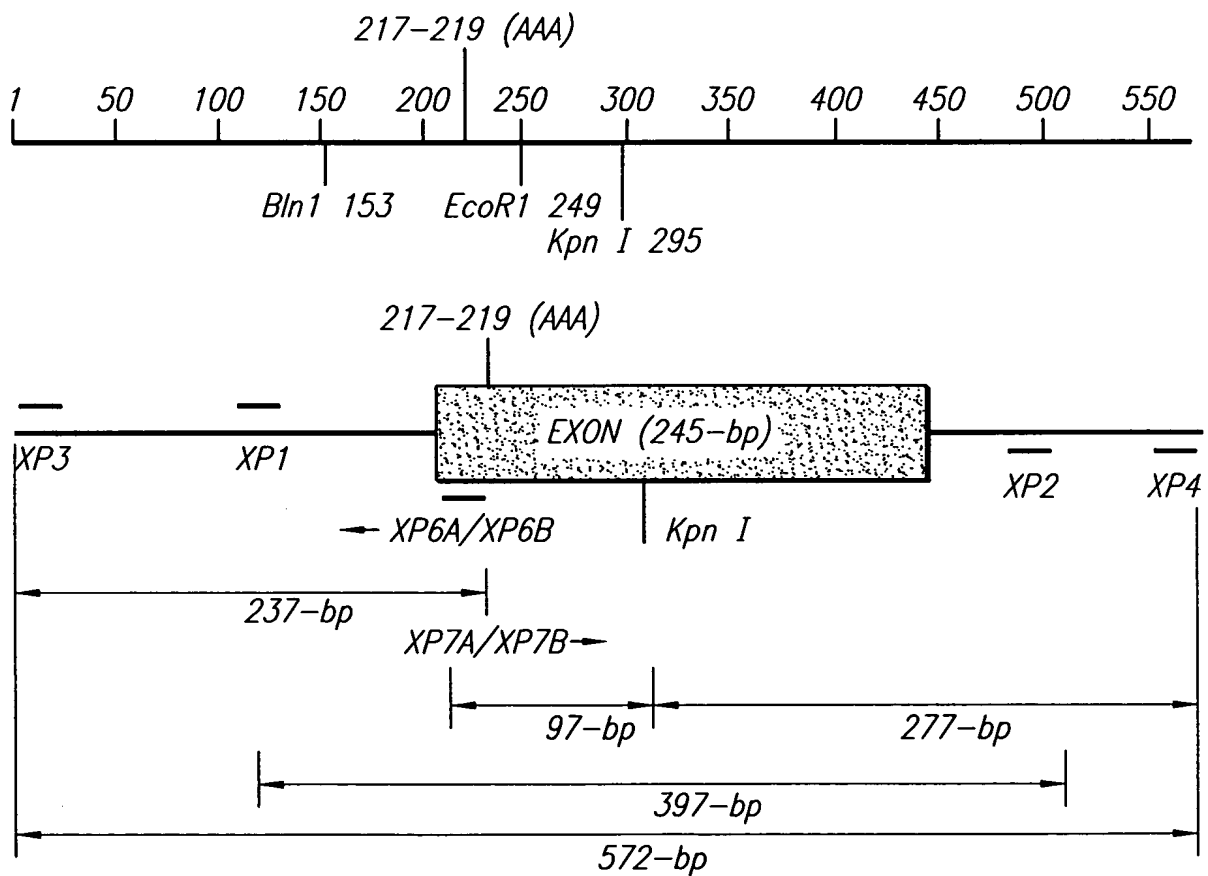
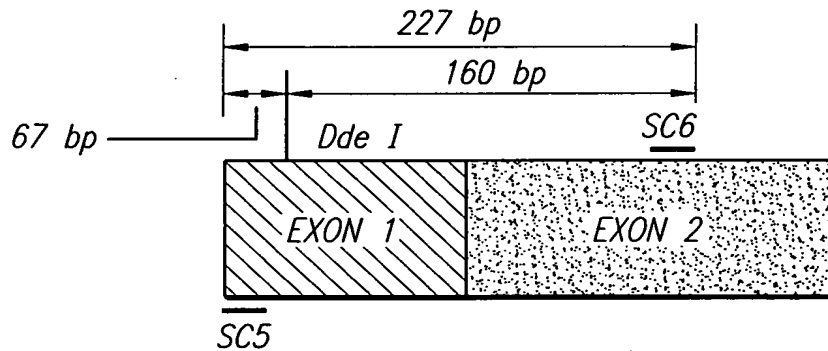


FIG. 21

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FIG. 22

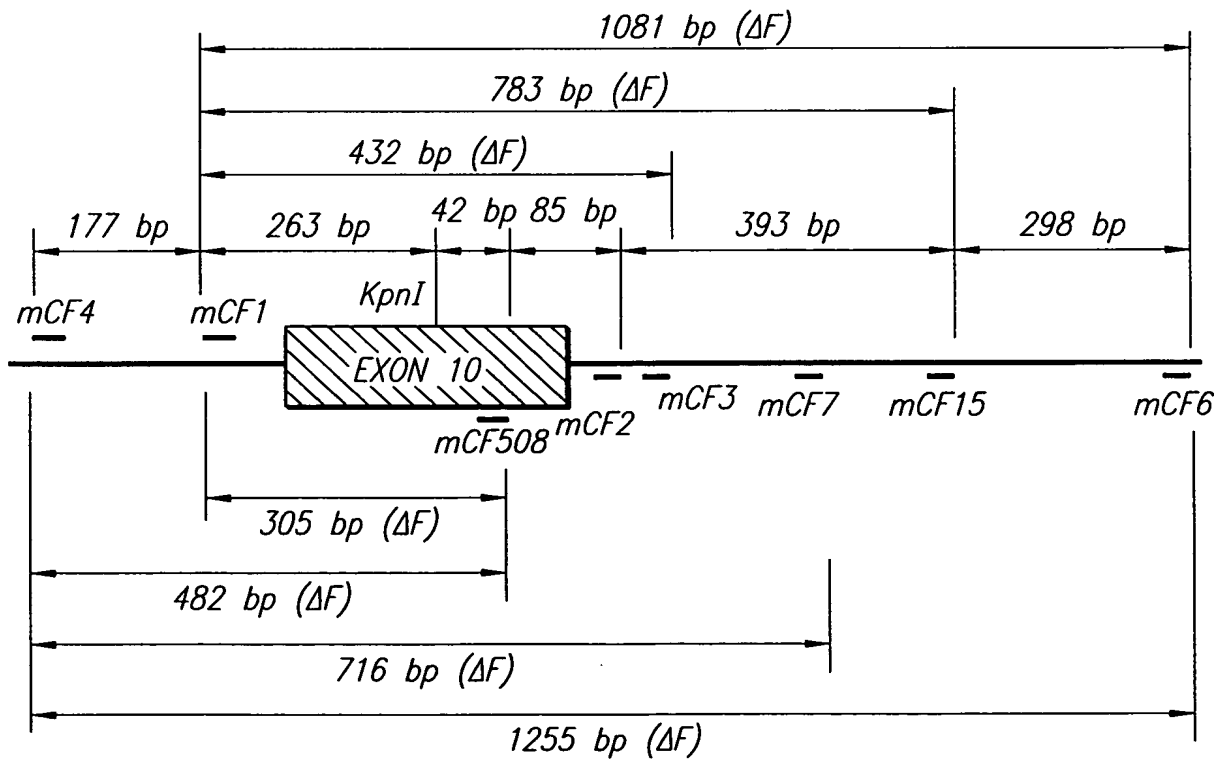
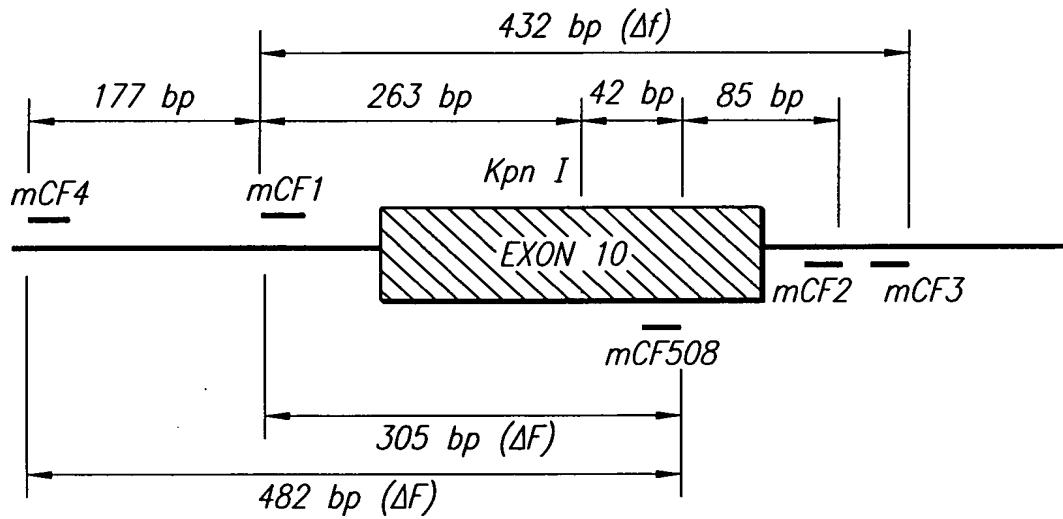
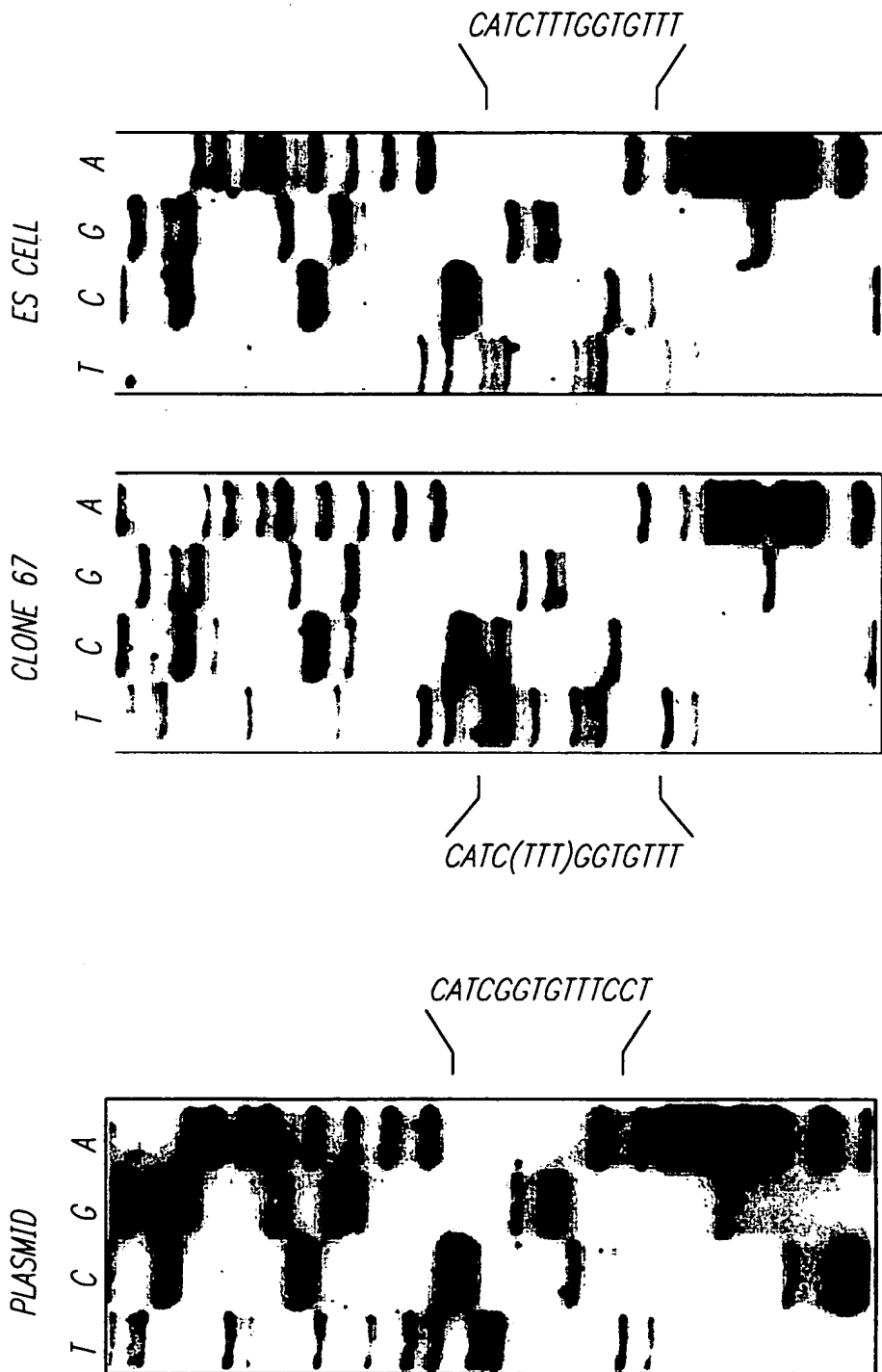


FIG. 23

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIG. 26



SEQ ID NO:87

SEQ ID NO:86

666060" 28926660

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIG. 30A

GAATTCCAGC	CAGACGTGAT	GGCGGGTGCC	CGTAGTCCCA	GCTACTCGGG	AGGCTGAGGC	60
AGGAGAATGG	CGTGAACCCA	GGAGGCAGAA	CTTGCACTGA	GCCGAGATCG	CGCCACTGCA	120
CTCTAGCCTG	GGTGACAGAG	TGAGACTCTG	TCTCTAAATA	AATAAATAAA	TAAATAAATA	180
<u>AATAAATAAA</u>	ATCAGTGCTT	TTTCTTCCTC	TGCTACCTCC	TTTCCTTCTA	CTCAGTTTTA	240
GTCAGTAGTA	TTATCTTTTT	TCAGATTTAT	CTTTGTATTG	TTAAATCTGC	TTATGCTTCT	300
ATTACTTTAT	TTATTAGCTT	TAAATGATAC	CTTTTGACTT	TCAGCTTTTC	TTAATAAAGC	360
AATCAGCAAA	TTTCCTTTAC	ACTCCACACT	TATACCCCAT	TTCCTTTGTT	TGTTTATTTG	420
GTTTTTACTT	CTAACTTTTC	TTATTGTCAG	GACATATAAC	ATATTTAAAC	TTTGTTTTTTC	480
AACTCGAATT	CTGCCATTAG	TTTTAATTTT	TGTTACACAGT	TATATAAATC	TTTGTTCACT	540
GATAGTCCTT	TTGTACTATC	ATCTCTTAAA	TGACTTTATA	CTCCAAGAAA	GGCTCATGGG	600
AACAATATTA	CCTGAATATG	TCTCTATTAC	TTAATCTGTA	CCTAATAATA	TGAAGGTAAT	660
CTACTTTGTA	GGATTTCTGT	GAAGATTAAA	TAAATTAATA	TAGTTAAAGC	ACATAGAACA	720
GCACTCGACA	CAGAGTGAGC	ACTTGGCAAC	TGTTAGCTGT	<u>TACTAACCTT</u>	<u>TCCCATTCTT</u>	780
			<u>cactgtagct</u>	<u>gtactacctt</u>	<u>ccat</u>	
<u>CCTCCAACC</u>	TATTCCAAC	ATCTGAATCA	TGTGCCCCTT	CTCTGTGAAC	CTCTATCATA	840
<u>ctcctc</u>	
ATACTTGTCA	CACTGTATTG	TAATTGTCTC	TTTTACTTTC	CCTTGTATCT	TTTGTGCATA	900
.....	
GCAGAGTACC	TGAAACAGGA	AGTATTTTAA	ATATTTTGAA	TCAAATGAGT	TAATAGAATC	960
.....	
TTTACAAATA	AGAATATACA	CTTCTGCTTA	GGATGATAAT	TGGAGGCAAG	TGAATCCTGA	1020
.....	
GCGTGATTG	ATAATGACCT	AATAATGATG	GGTTTTATTT	CCAGACTTCA	CTTCTAATGA	1080
.....	
TGATTATGGG	AGAACTGGAG	CCTTCAGAGG	GTAAAATTAA	GCACAGTGGA	AGAATTTTCT	1140
.....	
TCTGTTCTCA	GTTTTCTCTG	ATTATGCCTG	GCACCATTAA	AGAAAATATC	ATCTTTGGTG	1200
.....	
TTTCCTATGA	TGAATATAGA	TACAGAAAGC	TCATCAAAGC	ATGCCAACTA	GAAGAGGTAA	1260
.....	
GAACTATGT	GAAAACCTTT	TGATTATGCA	TATGAACCCT	TCACACTACC	CAAATTATAT	1320
.....	
ATTTGGCTCC	ATATTCAATC	GGTAGTCTA	CATATATTTA	TGTTTCCTCT	ATGGGTAAGC	1380
.....	
TACTGTGAAT	GGATCAATTA	ATAAAACACA	TGACCTATGC	TTTAAGAAGC	TTGCAAACAC	1440
.....	
ATGAAATAAA	TGCAATTTAT	TTTTTAAATA	ATGGGTTTCT	TTGATCACAA	TAAATGCATT	1500
.....	
TTATGAAATG	GTGAGAATTT	TGTTCACTCA	TTAGTGAGAC	AAACGTCCTC	AATGGTTATT	1560
.....	
TATATGGCAT	GCATATAAGT	GATATGTGGT	ATCTTTTTTAA	AAGATACCAC	AAAATATGCA	1620
.....	
TCTTTAAAAA	TATACTCCAA	AAATTATTAA	GATTATTTTA	ATAATTTTAA	TAATACTATA	1680
GCCTAATGGA	ATGAGCATTG	ATCTGCCAGC	AGAGAATTAG	AGGGGTAAAA	TTGTGAAGAT	1740
ATTGTATCCC	TGGCTTTGAA	CAAATACCAT	ATAACTTCTA	GTGACTGCAA	TTCTTTGATG	1800
CAGAGGCAAA	ATGAAGATGA	TGTCATTACT	CATTTACAAA	CAATATTGGA	GAATGAGCTA	1860

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